SEQUENCE LISTING

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<120> CELL LINES AND HOST NUCLEIC ACIDS RELATED TO INFECTIOUS DI	SEASES
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POT/USOB/B/198

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PCT/USOB/B/14B.

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120

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PCT/US03/371.43

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840

900

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rrrussas/szins

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caccactggc acccagatta gcagtttcat cgggagacta gaaactaagt ctgcaatto	t 360
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PCT/USDB/BZJ.NB

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PETZUSOSZSSLUS

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PCT/USO3/3/143

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420

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PCT/USD3/37%

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PCT/USOS/37143

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perzusoazazaua

180

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			gacattctta			360
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PCT/USO3/37143

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cttaaacaa tgggtatttt aaagacagaa gttgaaggaa gtccaagtat ccaattttaa	180
gatgcctat tagagcagtt ataagagagt gtctctcttt ctctctcttc tttcttctc	240
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PCT/USC3/37143

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aatataaaca ttattaaagg ccatgctgta aaaatactaa ttgattttcc tgtgtagcag	660
ttacaataga acaacgatag atctctaagg ggagagtgaa aggacctcaa tttgagaaac	720
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catggtgccc ctcgcccaaa gtctgacagt ttgatatggt agagccagga atccatccca	720
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<211> 866

<212> DNA

<213> Canis familiaris

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<222> (1)..(866)

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PCT/USOB/BZAHB

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PCT/USCB/B7143

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                                                                     300
aaaaattttt tcttgcaggt atttataaca gcaatgatgt agcagtatca tttccaaatg
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tggtatctgg ctcaggatct agcactcctg tctccagttc tcatttacct cagcagtctt
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PCT/USD3/37143

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taaattccta taggaattta taagtatctc catttgtttt gacacgttag tggatataat	660
agacattttt atgtgatatt catgagaaag gacaaaagaa tacattggca ttaactgatt	720
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PCT/USDA/37193

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PCT/USOB/BF143

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<212> DNA

<213> Cercopithecus aethiops

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PCT/USO3/37143

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PCT/USOB/B714B

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<211> 906

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POT/USOS/SFLUS

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rct/usus/37143

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PCT/USCB/371.43

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POTZUSOS/37143

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420

480

540

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61

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PCT/USCB/B7143

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ccctgtttnc agtaacccta ttccctctct gtgtccctgg ataaagtgct gcnacaatgc	660
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PCT/USQ3/37143

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PCT/USG3/37113

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PCT/USDB/BZ14B

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PCT/USOS/S7143

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rct/usq3/37143

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DCT/USD3/37143

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PET/USGB/B/147143

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PCT/USO3/37143

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⁸⁵

PCT/USO3/3/143

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PCT/USD3/3/1/13

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# PCT/USO3/37143

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### PCT/USCS/SFALLS

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360

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aatgtgcaaa ttttcttaga tgtgatcgct tcattttctc ttacatttta gattggcagc
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## PCT/USD3/3/143

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### PCT/USGB/B714B

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# PCT/USDB/BZIVB

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# PCT/USA3/37143

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# PCT/USCS/37143

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                                                                  240
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gcttgcacat ttgagtttat tattccatcc ctgtattaca ataaatattc tttacataaa
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                                                                     120
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                                                                     420
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# PCT/USOB/BF148

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# PCT/USOS/37143

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cnngaacctg	gnnacgacnn	ncnaagnggc	ncaancence	cncaggcgnc	tenneencet	900
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                                                                      120
gactgggnag agctccagag ccccagcagc ccggctcaag gncccctgcg cataggcgcc
                                                                      180
ccaccgngac gncagggacg cgactnccgn gangccccgc gcgccgnnng ancccaggcg
                                                                      240
egggennaga etgngatenn ggagnngece ngngeennne ngaeggngeg nnnnggnggn
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ggctccggga cgcgggactg ggtagagctc cagagcccca gcagcccggc tcaaggtccc
                                                                     180
ctgcgcatag gcgccccacc gtgacgtcag ggacgcgact cccgcgatgc cccgcgcgcc
                                                                     240
                                                                     300
gtctgatccc aggcgcggc tcannntttt atctcggagt tcccctgcgc cttcctgacg
gtgcgttctg gcggcctcgg gcgcgggctc tgcgatcgga cagcctggag cctttggcct
                                                                     360
cgatttacat gggaggcccc tcgaaacagg gcacgtcact tgcccccggt cacctgcgga
                                                                     420
cggggagact ctcgggttga ctccaaggcc tgacattccc ctccggtttt caccgaggag
                                                                     480
gatgaggatg ttgtcaggag ctgcggcaag gctggaggag cttgcgttgn gtccacccnc
                                                                     540
ctetghacag geettageat neacceneag ttteteeett gaettntgaa ecenaactee
                                                                     600
ttacccccgc aagtnncnnc cctgtttnga ttgctgaaac tgcaagtgac ggaagantaa
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720

aatgtttgcc naagcntnat gcttnanggn ggntgccngg gtataaggtc angggttggg

# oct/uspa/azilpa

ggcccttnnc	cctgnngggt	nggcnttaag	ntaacccagg	gnncntggca	nttnantnnt	780
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nttannctnt	annccnnagg	gaaanccntn	gggtcttgtt	tngccctgna	aanacnatna	900
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		tctcggagtt				300
	_	gcgatcggac				360
		cacgtcactt				420
		gacattcccc				480
		ctggaggagc				540
		ttctccctga		_		600
		tgaactgcaa				660
						720
•		ggntagaggt				780
_		gcactgantn				
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<211>

951

<212> DNA <213> Cercopithecus aethiops

¹²⁵ 

### PCT/USOB/B714B

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gggactgggt agageteeag ageeceagea geeeggetea aggteecetg egeataggeg
                                                                  180
                                                                   240
ccccaccgtg acgtcaggga cgcgactccc gngatgcccc gcgccgtc tgatcccagg
egegggetea nanttnnate teggagttee cetgegeett eetgaeggtg egttetggeg
                                                                   300
                                                                   360
gcctcgggcg cgggctctgc gatcggacag cctggagcct ttggcctcga tttacatggg
                                                                   420
aggecetteg aaacagggea egteaettge eeceggteae etgeggaegg ggagaetete
gggttgactc caaggcctga cattcccctc cggttttcac cgaggaggat gaggatgttg
                                                                   480
                                                                   540
tcaggagctg cggcaaggct ggaggagctt gcgttgggtc cacccgcctc tggacaggcc
ttagcattca cccgcagttt ctccctgact ttgaacccaa actccctacc cccgcaagtc
                                                                   600
cttccctgtt tgattgctga actgcaagtg acggaagaat taagtgttgg cgaaagctga
                                                                   660
                                                                   720
tgcttcaggg ggntgcaggg tagaggtcag gggtgggggc ctcgccttgt ggngtgcata
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ttcttagaaa atatcccctn tgnanctgnt acctgagnaa ccgctgggct ggcatnacct
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tgnaaaaccc agaanggtta nngccctttc ttantngtgg cccnattttt tcaggacnaa
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<222>
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                                                                  120
180
acticttgttg cccaggitgg agtacaatgg cacaatiting gittaccaca acctitiget
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cnnnttttca agcaattttt ntnncttann ctccctagta gctgggatta taggcatgtg

300

# PCT/USDS/37143

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ctacaggtac	acaccaccat	gtcagnctaa	tttttttt	tttttttt	ttgaaaccna	660
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ntncactnnt	nnactantct	ttttccacnt	attcttctct	nennetntne	tnatatenen	900
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	•					180
	acacaccca					240
	ccttttcacc					300
	caagagggac					
	ggctccagct					360
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canttcaact	ncgctaatta	acggaacagc	aggctngnaa	ttctgacaac	agcaggacac	180
aaanggggcn	gggatcagca	ctgaatgccg	gcgaagcatg	cencecece	ttaagaagaa	240
gćácáacacc	cacgacccac	attnnntntn	gggncaggtc	catgaaggng	cnaccctnga	300
tttagttana	ngenetnece	tgcagcaact	ccaagggcnc	agggttttta	aaatgncncc	360
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a	aacaggnct	gngattggtc	nagagcagga	nncgcccagc	centtnggct	ccccngggcc	480
а	cacngnaag	aaaaagaatn	gnnttggacc	acacagaaaa	cacaccaana	ctaangacag	540
С	tgaaaagct	caaaaaaaaa	atcgcnaaaa	aatccctcaa	tgctcnaaga	agtccncaaa	600
n	ncgccgngn	gacngnnaca	cagetneeng	gccngcanga	cnncnggggn	ncacaggnng	660
С	nacacccag	gaccagnagn	taatatcnna	aaagggtaac	aanaaaancc	ctaataccaa	720
а	aangcnatg	anaatggaag	cnnnacntcc	tncaaaagac	aagccctang	gaaancntcn	780
C	ncnacccnn	nccccaaccn	ggcanncggg	ccccaccca	aaaggggggn	nccgccccgg	840
a	annnaaaan	ccnacnnngg	ggaaaaanng	accnnaancc	ngaaanngtc	tatancccca	900
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<210> 196

<211> 868

<212> DNA

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<222> (1)..(868)

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ccctcccca ccctcatccc actccacngn taagagagag aaatnncagc actgntat	cc 180
tgnnnnatna tacatttncc ctnnngagtn aaggatnnna agatnnngaa agnaacag	aa 240
nagaaaccaa atntttttt	260
<210> 198 <211> 901 <212> DNA <213> Cercopithecus aethiops  <220> <221> misc_feature <222> (1)(901)	
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ccctcatccc actccactgc taagagagag aaatttnggc actgctatcc tgttntat	na 180
tacatntțcc cttttgagtn aaggattnna agattntgaa agtaacagaa tagaaacc	aa 240
aagtttnctc aactnccaan nnggctaaaa agagagaaat aatnattatt tcctatgn	na 300
cccaaaactn anncngnnaa taacagntat aattatatat ncaaatcaat aaatgaag	an 360
cgccaaaatc accttaatat aattgncagc agctaaagaa caaaaanncn ncncannn	gc 420
nncnataagn anacatcaca tgatnactnc tatngaccag naagaaacta gnaaaanca	ag 480
gcagncaccc acccacnenn nnctaacatt ennnnnenna nnenanceaa cetnnnne	gg 540
natatnenna agaageeaaa neaagaaaan nagacennea ngeenaaaaa aaaaengng	gn 600
nancnnaaac atcangaaca ggaaaccagn ngnaaaataa cacagggnat ncaaaagc	nn 660

# PCT/USO3/37X43

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gaaaacenga aanneeengg nnaaneeegg eanenneee caateeacaa eeeeeggna 780
naaneneeen aaaceeanee aaaacanaaa accengngge naaaaaaggen eeeenaaaaa 840
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<210> 199

<211> 885

<212> DNA

<213> Cercopithecus aethiops

<220>

<221> misc_feature

<222> (1)..(885)

<223> n is a, g, c or t

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<212> DNA

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cccaccctca tcccactcca cngntaagag agagaaattt cagcactgct atcctgtttt
                                                                     180
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gaagatcgcc aaaatcacct taatataatn gncagcanan aaagaacaaa aatnctttca
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gcctaannan nancgaggna atgcnnnncc caannttnaa caggnatncc nggcagngnt
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tntaacanng annatttcan angnnnnanc cggnaatact nnnanaannc cnannaaann
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naaaggnnan tcnnaatnca angttnaana aaangnaatn cncccnnnnn antantaaat
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aangnennna ntannannnn netaneaten enenenatge aennnnnaaa ntnnnnnntn
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agaacagcct tagcgaaagg cttcttgaag ggaaagatgt aactctgtga gatgaattca
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cagaacacaa agcagttttt ttagaaagct tctttctagt tttgatctga gaatatttcc
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# PCT/USO3/37143

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agagaaaata	gctttctntt	cancttncca	cgccttncct	gccaaaaatn	ccaanaaaaa	660
ancaatngng	nngnggngcc	ncgnntnntg	nngnttngng	tgtnccntgn	nctntccnan	720
tcccnntnag	ggnnaacnaa	tttttncnga	ctttaanaaa	naaaanaaaa	aanngnncaa	780
accaenttnn	aaactnnttt	aaanntncca	tnnnaaacct	taaancnnaa	aaccaaaaaa	840
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<211> 925

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<222> (1)..(925)

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120

925 atconnente nnetectent etcen 203 <210> 895 <211> <212> DNA Cercopithecus aethiops <213> <220> <221> misc_feature <222> (1)..(895) <223> n is a, g, c or t <400> 203 tttttcgng gattnctnnt ntnnnntnn ntccccccat tnnncttggg gggnaannnc 60 nacgattcan gtnttatnnc tacgaacaac cattgtgagt agaaccatct ggattttnca 120 180 tcactttcat ttaaaagact ctgttgatat tctaggtact gattccatat atcagtatca acaaatttct caaccaaggg gataattggt ttatctgttt gcaattcatt ccgtaattta 240 gaaaggagan anntttettt etttteaget teeaegeett eetgeaaaaa tacaagaaaa 300 360 atcaattgtg tgtgtgtctg tgtctgtgtt tgtgtgtgcn tgtctatgca attcctctag 420 qqtaacatat ttttacagac ttaagaagaa aagaaaaatg ttcaaactac attatacttc 480 tttaaacatt acatttagaa ctcttaaact gaaaatcaaa aaacacacac agatctcata 540 tgaacataat catgccttat ctatctaagt tctggccttt ctgtgtcttc ggtgatcatt actacagagg gaaaggaacc cctgacagat tttccatgtn ttttcatgct tccatacaca 600 ttnttctttc accattgaca ccnactanaa aaagaaaccn gtggnccttt ctgaggtttt 660 ttttttngnn anntnaattn nttttttta aacttggntt ttccncctna attnttancn 720 taggntnana aaangaaana ntgcctnnna tnaaaanggn ncctncaatn ntatnttacn 780 cnnanaagnc cnattggnna gggngcanaa antntnanng ggnnacnaaa ataaaannaa 840 895 aaataactct nnnanccttt ggttttacat taacnaaana nntctncccc caana

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gcatggcact	acattctctg	gccctttatc	agcactctga	cagctctctc	ctttgcttat	180
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ccttcacttt	gcattngncc	attgngtaac	atcacttaca	taccttnaat	tnttagttna	420
ttaattcata	ctgcaaaaca	acttantttt	taccatgtgc	caggcattgn	ccctagttgc	480
tgacaataca	gnngaaaata	aaatagacaa	aaatcccatc	tttngaatct	ttngaacctt	540
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gagaatacag	annngngngn	nnnnacnac	ngnateteen	gacaatagcn	cccannacan	720
		tnnaaaaang anaanaccca				780 840
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<210> 205 <211> 843

<211> 643 <212> DNA

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# PCT/USDB/B/B/L43

ncanatataa atgnncaaag agncnggcna cccnccccgn naanaaggnn agggncnctg 720
nnggccnaaa nnaggnnngg aagcaccnaa anaannngaa anaacccccc accaaaaccc 780
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 ctagcaatan ttcggttctt ccctcttgct ctcgggcgga ttcctgaaag tcgtttattc
                                                                       180
 tottaattaa tacgoogoto cagoocogoo ogttoagoto attotottaa togoattaco
                                                                       240
 ctggctgcng nnnctttttt ttttttccac ctgctgccac ccacccagac accgcctncg
                                                                       300
                                                                       360
 getettteeg gaccatetea gttteteete etteecengn eccaatttte tttaggetat
 ttctggctcc cgtaggtttn tcatgctctc gttagcccca ccccatcacc accancggct
                                                                       420
 ctttttcggc tctctcccgn cncctcctgt ctcctgctca ggctcttttc cagctattnn
                                                                       480
 cgactccct cntactcacc ctttgccttc ngaaactntc ccaccngccc ttcaggcaaa
                                                                       540
 tengtetena ecceetante eegeaegtga acacagneet neceeteeg eettettaga
                                                                       600
 nacccctct caccnnnncc ctttccnncc catcctcaaa actananggn tgggtacngg
                                                                       660
                                                                       720
 conancence entittggtg nnnaanneen gaategeegn caaggneeg ginenineee
                                                                       780
 ngaaaancet atngnenggn cacaaacang ggaaacannn ttencaceen ttntccactg
                                                                       840
 ancenettee ecenteacce ttnaaanaca ttntttnnnt ttatetaaaa centteanee
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                                                                      120
 gctccaacca gcctcagatt ggttcgcttg aatcttaaaa ttacttttct ggtcacgcgc
                                                                      180
gccgaaggtc taagcatttg tgaaatgtct tttttccccc cccccacccc ttgatgctgt
                                                                      240
 tctctttggn nttttttaat tacacagggg ttgagaaacc aaattaaaat taggcgtgtc
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agtgttggca	ggtggagaat	gctaccgcag	ccgcccagac	agatctgcag	actggcccca	540
ttgcagagga	ttagacacag	ggtgcgtgga	tcatagggtt	tttgtacaga	angcagtttt	600
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ggggttcana	aagnacgttg	ctngccatct	tnggaggttt	cctgctcact	tntcaaangg	720
ncaggctngc	cttttaaaaa	tcaatgttcc	ttccaccccc	aaaagggntt	ctttttgcag	780
tgaatcanct	nccaaaataa	atagcccccn	tttttttgga	aaagaacgtt	tgnaaatccc	840
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# POT/USOB/B7143

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cacttattat ctctcatggt tctgtgtgtt gactagacat ttcggctcct gtgcagatgg
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                                                                      300
gagcattgta atantgagca tttcaacagt attaacccaa catgcaaaca ctcactatag
                                                                      420
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                                                                      480
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                                                                      540
                                                                    (600
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                                                                      660
aaaaanaaaa ttnggaagaa aggggccnca agccaaggga atnccaggca tttcnctaan
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tnggccaaaa caanannatn aaaantcntc ccccnnnnnc cnncnanaaa aaantgnaac `
                                                                      780
                                                                      840
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ccattaacag ttttactcgc agcctctgct tngtctacat ctgctgccaa cttttaacta
atggcgagat actttcgcta tttccgatgc cattaggaaa caaatagaaa aatagtttgg
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```

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cgcgcccgcc	tgtaatccgg	gaatcccagc	gttttgcgag	cccacgccca	ggccgaggag	420
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# PCT/USOB/BFAUB

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¹⁴¹ 

# PCT/USDB/37143

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tgagctagcc cttaagtaac gccattttgc aaggcatgga aaaatacata actgagaata 180
gaaaagttca gatcgaggtc aggaacagat ggaacagggt cgaccggtcg accggtcgac 24
cctagagaac nnttttntgt ttccagggtg ccccaaggac ctgaaatgac cctgtgcctt 30
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aagccccttt tcnactccnt gggncctttt ngtnnttntc ttgnccacct ttcttgactt 84
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aatctggggc ccatcagccc ccactgccct tcctggtacc ctgagcatgc tggcaagggg 18
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# PCT/USC3/37143

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#### PCT/USOB/B7143

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				Asn	Gln	Leu	Leu	tat Tyr	Ser	Gln	Arg	Arg	Ala				、1160
								aaa Lys 300									1208
								gga Gly									1256
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								gaa Glu									1400

## PCT/USDB/B714B

360 365 370	
gtg cag cat caa ttg ctt gta att ctt aag gag ctc cga aaa gca aga Val Gln His Gln Leu Leu Val Ile Leu Lys Glu Leu Arg Lys Ala Arg 375 380 385	1448
aat caa ata aca cag ttg gaa tcc ttg aaa cag ctt cat gag ttt gcc Asn Gln Ile Thr Gln Leu Glu Ser Leu Lys Gln Leu His Glu Phe Ala 390 395 400	1496
atc aca gag cca tta gtc act ttc caa gga gag act gaa aac aga gaa Ile Thr Glu Pro Leu Val Thr Phe Gln Gly Glu Thr Glu Asn Arg Glu 405 410 415 420	1544
aaa gtt gcc gcc tca cca aaa agt ccc act gct gca ctc aat gaa agc Lys Val Ala Ala Ser Pro Lys Ser Pro Thr Ala Ala Leu Asn Glu Ser 425 430 435	1592
ctg gtg gaa tgt ccc aag tgc aat ata cag tat cca gcc act gag cat Leu Val Glu Cys Pro Lys Cys Asn Ile Gln Tyr Pro Ala Thr Glu His 440 445 450	1640
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<213> homo sapiens

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Gly Lys Leu Thr Asp Lys Glu Arg His Arg Leu Leu Glu Lys Ile Arg 50 55 60

Val Leu Glu Ala Glu Lys Glu Lys Asn Ala Tyr Gln Leu Thr Glu Lys 65 70 75 80

Asp Lys Glu Ile Gln Arg Leu Arg Asp Gln Leu Lys Ala Arg Tyr Ser 85 90 95

Thr Thr Ala Leu Glu Glu Glu Glu Glu Thr Thr Arg Glu Gly Glu
100 105 110

Arg Arg Glu Gln Val Leu Lys Ala Leu Ser Glu Glu Lys Asp Val Leu 115 , 120 125

Lys Gln Gln Leu Ser Ala Ala Thr Ser Arg Ile Ala Glu Leu Glu Ser 130 135 140

Lys Thr Asn Thr Leu Arg Leu Ser Gln Thr Val Ala Pro Asn Cys Phe 145 150 155 160

Asn Ser Ser Ile Asn Asn Ile His Glu Met Glu Ile Gln Leu Lys Asp 165 170 175

Ala Leu Glu Lys Asn Gln Gln Trp Leu Val Tyr Asp Gln Gln Arg Glu 180 185 190

Val Tyr Val Lys Gly Leu Leu Ala Lys Ile Phe Glu Leu Glu Lys Lys 195 200 205

Thr Glu Thr Ala Ala His Ser Leu Pro Gln Gln Thr Lys Lys Pro Glu 210 215 220

Ser Glu Gly Tyr Leu Gln Glu Glu Lys Gln Lys Cys Tyr Asn Asp Leu 225 230 235 240

Leu Ala Ser Ala Lys Lys Asp Leu Glu Val Glu Arg Gln Thr Ile Thr 245 250 255

Gln Leu Ser Phe Glu Leu Ser Glu Phe Arg Arg Lys Tyr Glu Glu Thr 260 265 270

Gln Lys Glu Val His Asn Leu Asn Gln Leu Leu Tyr Ser Gln Arg Arg 275 280 285

Ala Asp Val Gln His Leu Glu Asp Asp Arg His Lys Thr Glu Lys Ile 290. 295 300 (

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Thr Ser Leu Leu Lys Gln Gln Glu Glu Gln Thr Arg Val Ala Leu Leu 340 345 350

Glu Gln Gln Met Gln Ala Cys Thr Leu Asp Phe Glu Asn Glu Lys Leu 355 360 365

Asp Arg Gln His Val Gln His Gln Leu Leu Val Ile Leu Lys Glu Leu 370 375 380

Arg Lys Ala Arg Asn Gln Ile Thr Gln Leu Glu Ser Leu Lys Gln Leu 385 390 395 400

His Glu Phe Ala Ile Thr Glu Pro Leu Val Thr Phe Gln Gly Glu Thr 405 410 415

Glu Asn Arg Glu Lys Val Ala Ala Ser Pro Lys Ser Pro Thr Ala Ala 420 425 430

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## PCT/USOS/S7143

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						tat Tyr										872
						ttt Phe										920
						cag Gln										968
						aaa Lys 235										1016
aaa Lys 245	aaa Lys	gat Asp	ctt Leu	gag Glu	gtt Val 250	gaa Glu	cga Arg	caa Gln	acc Thr	ata Ile 255	act Thr	cag Gln	ctg Leu	agt Ser	ttt Phe 260	1064
gaa Glu	ctg Leu	agt Ser	gaa Glu	ttt Phe 265	cga Arg	aga Arg	aaa Lys	tat Tyr	gaa Glu 270	gaa Glu	acc Thr	caa Gln	aaa Lys	gaa Glu 275	gtt Val	1112
						ttg Leu										1160
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tcc Ser 325	gaa Glu	gag Glu	ctc Leu	tta Leu	tct Ser 330	cag Gln	gtc Val	cag Gln	ttt Phe	ctt Leu 335	tac Tyr	aca Thr	tct Ser	ctg Leu	cta Leu 340	1304
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cag Gln	gca Ala	tgt Cys	act Thr 360	tta Leu	gac Asp	ttt Phe	gaa Glu	aat Asn 365	gaa Glu	aaa Lys	ctc Leu	gac Asp	cgt Arg 370	caa Gln	cat His	1400
						gta Val										1448
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## PCT/USG3/37143

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cgc gat ctg ctt gtc cat gtg gaa tac tgt tca aag tag caaaataagt Arg Asp Leu Leu Val His Val Glu Tyr Cys Ser Lys 455 460	1689
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<400> 230

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- Gly Lys Leu Thr Asp Lys Glu Arg His Arg Leu Leu Glu Lys Ile Arg 50 55 60
- Val Leu Glu Ala Glu Lys Glu Lys Asn Ala Tyr Gln Leu Thr Glu Lys 65 70 75 80
- Asp Lys Glu Ile Gln Arg Leu Arg Asp Gln Leu Lys Ala Arg Tyr Ser 85 90 95
- Thr Thr Ala Leu Leu Glu Gln Leu Glu Glu Thr Thr Arg Glu Gly Glu
  100 105 110
- Arg Arg Glu Gln Val Leu Lys Ala Leu Ser Glu Glu Lys Asp Val Leu 115 120 125
- Lys Gln Gln Leu Ser Ala Ala Thr Ser Arg Ile Ala Glu Leu Glu Ser 130 135 140
- Lys Thr Asn Thr Leu Arg Leu Ser Gln Thr Val Ala Pro Asn Cys Phe 145 ' 150 155 160
- Asn Ser Ser Ile Asn Asn Ile His Glu Met Glu Ile Gln Leu Lys Asp 165 170 175
- Ala Leu Glu Lys Asn Gln Gln Trp Leu Val Tyr Asp Gln Gln Arg Glu 180 185 190
- Val Tyr Val Lys Gly Leu Leu Ala Lys Ile Phe Glu Leu Glu Lys Lys 195 200 205
- Thr Glu Thr Ala Ala His Ser Leu Pro Gln Gln Thr Lys Lys Pro Glu 210 215 220
- Ser Glu Gly Tyr Leu Gln Glu Glu Lys Gln Lys Cys Tyr Asn Asp Leu 225 230 235 240
- Leu Ala Ser Ala Lys Lys Asp Leu Glu Val Glu Arg Gln Thr Ile Thr 245 250 255
- Gln Leu Ser Phe Glu Leu Ser Glu Phe Arg Arg Lys Tyr Glu Glu Thr 260 265 270

Gln Lys Glu Val His Asn Leu Asn Gln Leu Leu Tyr Ser Gln Arg Arg 275 280

Ala Asp Val Gln His Leu Glu Asp Asp Arg His Lys Thr Glu Lys Ile 290 295

Gln Lys Leu Arg Glu Glu Asn Asp Ile Ala Arg Gly Lys Leu Glu Glu 315

Glu Lys Lys Arg Ser Glu Glu Leu Leu Ser Gln Val Gln Phe Leu Tyr

Thr Ser Leu Leu Lys Gln Gln Glu Glu Gln Thr Arg Val Ala Leu Leu

Glu Gln Gln Met Gln Ala Cys Thr Leu Asp Phe Glu Asn Glu Lys Leu

Asp Arg Gln His Val Gln His Gln Leu Leu Val Ile Leu Lys Glu Leu

Arg Lys Ala Arg Asn Gln Ile Thr Gln Leu Glu Ser Leu Lys Gln Leu 390 395

His Glu Phe Ala Ile Thr Glu Pro Leu Val Thr Phe Gln Gly Glu Thr 405 410

Glu Asn Arg Glu Lys Val Ala Ala Ser Pro Lys Ser Pro Thr Ala Ala 420 425

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Ala Thr Glu His Arg Asp Leu Leu Val His Val Glu Tyr Cys Ser Lys 455

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<211> 6829

<212> DNA

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<220>

<221> CDS <222> (89)..(6274)

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								aaa Lys										160
S								aaa Lys										208
_		_			_			gag Glu		_			_					256
								tcc Ser										304
								tta Leu 80										352
								agc Ser										400
S		_						caa Gln										448
_	-				-	_		tct Ser	_					-				496
								gga Gly										544
_		_	-		-			gca Ala 160								_		592
								gct Ala										640
V	ta al 85	aag Lys	aac Asn	agc ['] Ser	cgg Arg	cgg Arg 190	atg Met :	ctg Leu	tca Ser	aat Asn	aag Lys 195	cca Pro	cag Gln	gac Asp	ttc Phe	cag Gln 200		688
								ggc Gly									,	736
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а	tc	aag	aga	gga	aac	aac	cct	ttt	ttt	gat	gag	ttg	ttt	ttc	tac	aat	;	832

	Ile	Lys	Arg 235	Gly	Asn	Asn	Pro	Phe 240	Phe	Asp	Glu	Leu	Phe 245	Phe	Tyr	Asn	
,	gtc Val	aac Asn 250	atg Met	acc Thr	cct Pro	tct Ser	gaa Glu 255	ttg Leu	atg Met	gat Asp	gag Glu	atc Ile 260	atc Ile	agc Ser	atc Ile	cgg Arg	880
,												ctg Leu					928
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	aca Thr	ata Ile	tat Tyr	gac Asp	tgg Trp 445	gac Asp	cgt Arg	ctt Leu	act Thr	aaa Lys 450	aat Asn	gat Asp	gta Val	gtt Val	gga Gly 455	aca Thr	1456
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												tat Tyr					1552

		475					480					485					
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aat Asn 505	ctt Leu	tat Tyr	gga Gly	agc Ser	ccc Pro 510	agg Arg	gag Glu	tac Tyr	acg Thr	gga Gly 515	ttc Phe	cca Pro	gac Asp	ccc Pro	tat Tyr 520	164	3
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cag Gln	cga Arg 570	agg Arg	cgg Arg	aag Lys	tac Tyr	agc Ser 575	ctg Leu	tct Ser	gcc Ala	gtg Val	ttt Phe 580	cat His	tca Ser	gcc Ala	acc Thr	184	0
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aac Asn	tat Tyr	ggc Gly	aac Asn	aag Lys 605	ttt Phe	gac Asp	acc Thr	acc Thr	tgt Cys 610	aag Lys	cct Pro	ttg Leu	gca Ala	tca Ser 615	aca Thr	193	6
act Thr	cag Gln	tac Tyr	agc Ser 620	cgt Arg	gct Ala	gta Val	ttt Phe	gat Asp 625	ggc	aac Asn	tac Tyr	tat Tyr	tat Tyr 630	tac Tyr	ttg Leu	198	4
cct Pro	tgg Trp	gcc Ala 635	cac His	acc Thr	aag Lys	cca Pro	gtt Val 640	gtt Val	acc Thr	ctg Leu	act Thr	tca Ser 645	tac Tyr	tgg Trp	gag Glu	203	2

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# PCT/USOB/B714

tgt Cys	cct Pro 970	cca Pro	ggt Gly	tgg g Trp G	3lu 1	gg g rp 6	gaa g Slu <i>l</i>	gat g Asp <i>A</i>	gat go Asp Al	a to la Tr 98	p Se	et ta er Ty	it ga vr As	ac ata sp Ile		3040
aat Asn 985	cga Arg	gcg Ala	gtg Val	Asp (	gag a Slu I 990	aaa g Lys (	gc ( Sly (	tgg g Frp (	gaa ta Slu Ty 99	r Gl	ga at ly Il	c ac le Th	ec at	t cct le Pro 1000	)	3088
cct Pro	gat Asp	cat His	aag Lys	ccc Pro 1005	aaa Lys	tcc Ser	tgg Trp	gtt Val	gca Ala 1010	gca Ala	gag Glu	aaa Lys	atg Met	tac Tyr 1015		3133
cac His	act Thr	cat His	aga Arg	cgg Arg 1020	cga Arg	agg Arg	ctg Leu	gtc Val	cga Arg 1025	aaa Lys	cgc Arg	aag Lys	aaa Lys	gat Asp 1030		3178
tta Leu	aca Thr	cag Gln	act Thr	gct Ala 1035	tca Ser	agc Ser	acc Thr	gca Ala	agg Arg 1040	gcc Ala	atg Met	gag Glu	gaa Glu	ttg Leu 1045		3223
caa Gln	gac Asp	caa Gln	gag Glu	ggc Gly 1050	tgg Trp	gaa Glu	tat Tyr	gct Ala	tct Ser 1055	cta Leu	att Ile	ggc Gly	tgg Trp	aaa Lys 1060		3268
ttt Phe	cac His	tgg Trp	aaa Lys	caa Gln 1065	cgt Arg	agt Ser	tca Ser	gat Asp	acc Thr 1070	ttc Phe	cgc Arg	cgc Arg	aga Arg	cgc Arg 1075		3313
tgg Trp	agg Arg	aga Arg	aaa Lys	atg Met 1080	gct Ala	cct Pro	tca Ser	gaa Glu	aca Thr 1085	cat His	ggt Gly	gca Ala	gċt Ala	gcc Ala 1090		3358
atc Ile	ttt Phe	aaa Lys	ctt Leu	gaa Glu 1095	ggt Gly	gcc Ala	ctt Leu	GJÀ aga	gca Ala 1100	gac Asp	act Thr	acc Thr	gaa Glu	gat Asp 1105		3403
ggg	gat Asp	gag Glu	aag Lys	agc Ser 1110	ctg Leu	gag Glu	aaa Lys	cag Gln	aag Lys 1115	cac His	agt Ser	gcc Ala	acc Thr	act Thr 1120		3448
gtg Val	ttc Phe	gga Gly	gca Ala	aac Asn 1125	acc Thr	ccc Pro	att Ile	gtt Val	tcc Ser 1130	tgc Cys	aat Asn	ttt Phe	gac Asp	aga Arg 1135		3493
gtc Val	tac Tyr	atc Ile	tac Tyr	cat His 1140	ctg Leu	cgc Arg	tgc Cys	tat Tyr	gtc Val 1145	tat Tyr	caa Gln	gcc Ala	aga Arg	aac Asn 1150		3538
ctc Leu	ttg Leu	gct Ala	tta Leu	gat Asp 1155	aag Lys	gat Asp	agc Ser	ttt Phe	tca Šer 1160	gat Asp	cca Pro	tat Tyr	gct Ala	cat His 1165		3583
atc Ile	tgt Cys	ttc Phe	ctc Leu	cat His 1170	cgg Arg	agc Ser	aaa Lys	acc Thr	act Thr 1175	gag Glu	atc Ile	atc Ile	cat His	tca Ser 1180		3628
acc Thr	ctg Leu	aat Asn	ccc Pro	acg Thr 1185	tgg Trp	gac Asp	caa Gln	aca Thr	att Ile 1190	ata Ile	ttc Phe	gat Asp	gaa Glu	gtt Val 1195		3673
gaa	atc	tat	ggg	gaa	ccc	caa	aca	gtt	cta	cag	aat	cca	ccc	aaa		3718

Glu	Ile	Tyr	Gly	Glu 1200	Pro	Gln	Thr	Val	Leu 1205	Gln	Asn	Pro	Pro	Lys 1210	
gtt Val	atc Ile	atg Met	gaa Glu	ctt Leu 1215	ttt Phe	gac Asp	aat Asn	gac Asp	caa Gln 1220	gtg Val	ggc Gly	aaa Lys	gat Asp	gaa Glu 1225	3763
ttt Phe	tta Leu	gga Gly	cga Arg	agc Ser 1230	att Ile	ttc Phe	tct Ser	cct Pro	gtg Val 1235	Val	aaa Lys	ctg Leu	aac Asn	tca Ser 1240	3808
gaa Glu	atg Met	gac Asp	atc Ile	aca Thr 1245	ccc Pro	aaa Lys	ctt Leu	ctc Leu	tgg Trp 1250	cac His	cca Pro	gta Val	atg Met	aat Asn 1255	3853
gga Gly	gac Asp	aaa Lys	gcc Ala	tgc Cys 1260	GJÀ āāā	gat Asp	gtt Val	ctt Leu	gta Val 1265	act Thr	gca Ala	gag Glu	ctg Leu	att Ile 1270	3898
ctg Leu	agg Arg	ggc Gly	aag Lys	gat Asp 1275	ggc Gly	tcc Ser	aac Asn	ctt Leu	ccc Pro 1280	att Ile	ctt Leu	ccc Pro	cct Pro	caa Gln 1285	3943
agg Arg	gcg Ala	cca Pro	aat Asn	cta Leu 1290	tac Tyr	atg Met	gtc Val	ccc Pro	cag Gln 1295	Gly	atc Ile	agg Arg	cct Pro	gtg Val 1300	3988
gtc Val	cag Gln	ctc Leu	act Thr	gcc Ala 1305	att Ile	gag Glu	att Ile	cta Leu	gct Ala 1310	Trp	ggc Gly	tta Leu	aga Arg	aat Asn 1315	4033
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gtg Val	gag Glu	tgt Cys	gga Gly	gga Gly 1335	gaa Glu	agg Arg	gtg Val	gaa Glu	tcg Ser 1340	Val	gtg Val	atc Ile	aaa Lys	aac Asn 1345	4123
ctt Leu	aag Lys	Lvs	Thr	ccc Pro 1350	Asn	Phe	Pro	Ser	Ser	Val	Leu	Phe	Met	aaa Lys 1360	4168
gtg Val	ttc Phe	ttg Leu	ccc Pro	aag Lys 1365	gag Glu	gaa Glu	ttg Leu	tac Tyr	atg Met 1370	Pro	cca Pro	ctg Leu	gtg Val	atc Ile 1375	4213
aag Lys	gtc Val	atc Ile	gac Asp	cac His 1380	agg Arg	cag Gln	ttt Phe	GJA āāā	cgg Arg 1385	Lys	cct Pro	gtc Val	gtc Val	ggc Gly 1390	4258
cag Gln	tgc Cys	acc Thr	atc Ile	gag Glu 1395	Arg	ctg Leu	gac Asp	cgc Arg	ttt Phe 1400	Arg	tgt Cys	gac Asp	cct Pro	tat Tyr 1405	4303
gca Alá	_GJA _aaa	aaa Lys	gag Glu	gac Asp 1410	atc Ile	gtc Val	cca Pro	cag Gln	ctc Leu 1415	Lys	gcc Ala	tcc Ser	ctt Leu	ctg Leu 1420	4348
tct Ser	gcc Ala	cca Pro	cca Pro	tgc Cys	cgg Arg	gac Asp	atc Ile	gtt Val	atc Ile	gaa Glu	atg Met	gaa Glu	gac Asp	acc Thr	4393

### PCT/USOB/B754F

	1425	1	430	1435
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aaa tgc gga cag Lys Cys Gly Gln		Lys Gly T	at tcc aag ctc aa yr Ser Lys Leu Ly 475	g ata 4528 s Ile 1480
tat aat tgt gaa Tyr Asn Cys Glu	cta gaa aat Leu Glu Asn 1485	Val Ala G	aa ttt gag ggc ct lu Phe Glu Gly Le 490	g aca 4573 1 Thr 1495
gac ttc tca gat Asp Phe Ser Asp	acg ttc aag Thr Phe Lys 1500	Leu Tyr A	ga ggc aag tcg ga rg Gly Lys Ser As 505	gaa 4618 Glu 1510
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aat ggc ctg tgt Asn Gly Leu Cys		Ile Lys I	ata aca ctg ggc aa [le Thr Leu Gly Ly 1580	a aaa 4843 s Lys 1585
gtc att gaa gac Val Ile Glu Asp	cga gat cac Arg Asp His 1590	Tyr Ile F	ccc aac act ctc aa Pro Asn Thr Leu As 1595	c cca 4888 n Pro 1600
gtc ttt ggc agg Val Phe Gly Arg	atg tac gaa Met Tyr Glu 1605	Leu Ser C	tgc tac tta cct ca Cys Tyr Leu Pro Gl 1610	a gaa 4933 n Glu 1615
aaa gac ctg aaa Lys Asp Leu Lys	att tct gtc lle Ser Val 1620	Tyr Asp T	tat gac acc ttt ac Tyr Asp Thr Phe Th 1625	c cgg 4978 r Arg 1630
gat gaa aaa gta Asp Glu Lys Val	gga gaa aca Gly Glu Thr 1635	Ile Ile A	gat ctg gaa aac cg Asp Leu Glu Asn Ar 1640	a ttc 5023 g Phe 1645
ctt tcc cgc ttt Leu Ser Arg Phe	ggg tcc cac Gly Ser His 1650	Cys Gly I	ata cca gag gag ta Ile Pro Glu Glu Ty 1655	c tgt 5068 r Cys 1660

#### PCT/USOB/B7 14B

gtt Val	tct Ser	gga Gly	gtc Val	aat Asn 1665	acc Thr	tgg Trp	cga Arg	gat Asp	caa Gln 1670	ctg Leu	aga Arg	cca Pro	aca Thr	cag Gln 1675	, 5	113
ctg Leu	ctt Leu	caa Gln	aat Asn	gtc Val 1680	gcc Ala	aga Arg	ttc Phe	aaa Lys	ggc Gly 1685	ttc Phe	cca Pro	caa Gln	ccc Pro	atc Ile 1690	5	158
ctt Leu	tcc Ser	gaa Glu	gat Asp	ggg Gly 1695	agt Ser	aga Arg	atc Ile	aga Arg	tat Tyr 1700	gga Gly	gga Gly	cga Arg	gac Asp	tac Tyr 1705	<del>-</del>	203
agc Ser	ttg Leu	gat Asp	gaa Glu	ttt Phe 1710	gaa Glu	gcc Ala	aac Asn	aaa Lys	atc Ile 1715	ctg Leu	cac His	cag Gln	cac His	ctc Leu 1720	5	248
Gl ^A aaa	gcc Ala	cct Pro	gaa Glu	gag Glu 1725	cgg Arg	ctt Leu	gct Ala	ctt Leu	cac His 1730	atc Ile		agg Arg			5	
Gly	ctg Leu	gtc Val	cct Pro	gag Glu 1740	cac His	gtg Val	gaa Glu	aca Thr	agg Arg 1745	act Thr	ttg Leu	cac His	agc Ser	acc Thr 1750	5	338
ttc Phe	cag Gln	ccc Pro	aac Asn	att Ile 1755	tcc Ser	cag Gln	gga Gly	aaa Lys	ctt Leu 1760	cag Gln	atg Met	tgg Trp	gtg Val	gat Asp 1765	5	383
gtt Val	ttc Phe	ccc Pro	aag Lys	agt Ser 1770	ttg Leu	ggg Gly	cca Pro	cca Pro	ggc Gly 1775	cct Pro	cct Pro	ttc Phe	aac Asn	atc Ile 1780	5	428
aca Thr	ccc Pro	cgg Arg	aaa Lys	gcc Ala 1785	aag Lys	aaa Lys	tac Tyr	Tyr	ctg Leu `1790	cgt Arg	gtg Val	atc Ile	atc Ile	tgg Trp 1795	5	473
				gtt Val 1800								aca Thr			5	5518
				atc Ile 1815								ggc Gly				5563
_		aaa Lys							tac Tyr 1835			ttg Leu		ggt Gly 1840	5	608
_		aat Asn		aac Asn 1845			ttt Phe		ttc Phe 1850			gac Asp			5	653
	•	gaa Glu		ctc Leu 1860					aaa Lys 1865	aaa Lys	gag Glu	cat His	ttc Phe	tgg Trp 1870	5	698
-		_		acg Thr 1875					cca Pro 1880			ctg Leu			5	743

## PCT/US03/37143

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cca Pro	gag Glu	aaa Lys	tgc Cys	agg Arg 1920	ttg Leu	gac Asp	atg Met	att Ile	ccg Pro 1925	gac Asp	ctc Leu	aaa Lys	gcc Ala	atg Met 1930	5878
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aac Asn	atg Met	aac Asn	ccc Pro	aag Lys 1995	Leu	gac Asp	tta Leu	cca Pro	aat Asn 2000	Arg	cca Pro	gaa Glu	acc Thr	tcc Ser 2005	6103
ttc Phe	ctc Leu	tgg Trp	ttc Phe	acc Thr 2010	Asn	cca Pro	tgc Cys	aag Lys	acc Thr 2015	Met	aag Lys	ttc Phe	atc Ile	gtg Val 2020	6148
tgg Trp	cgc Arg	cgc Arg	ttt Phe	aag Lys 2025	$\mathtt{Trp}$	gtc Val	atc Ile	atc Ile	ggc Gly 2030	Leu	ctg Leu	ttc Phe	ctg Leu	ctt Leu 2035	6193
ato Ile	ctg Leu	ctg Lev	rctc Leu	ttc Phe 2040	Val	gcc Ala	gtg Val	ctc Leu	ctc Leu 2045	JAI	tct Ser	ttg Leu	ccg Pro	aac Asn 2050	6238
tat Tyr	ttg Lev	tca Ser	atg Met	aag Lys 2055	Ile	gta Val	aag Lys	cca Pro	aat Asn 2060	Val	taa	caa	aggo	aaa	6284
ggo	cttca	attt	caag	Jagtca	at co	agca	atga	gag	gaatco	tg o	ctct	gtag	a co	aacatcca	6344
gto	gtgat	ttt	gtgt	ctgaç	ga co	cacac	ccca	gta	gcagg	gtt a	acgco	atgt	c ac	cgagcccc:	6404
att	tgatt	ccc	agag	ggtct	t ag	gtcct	ggaa	agt	caggo	cca a	acaag	gcaac	g tt	tgcatcat	6464
gti	tatct	ctt	aagt	attaa	aa ag	gttt	attt	tet	aaagt	tt a	aaato	atgt	t tt	tcaaaata	6524
tti	tttca	aagg	tgg	tggti	cc ca	attta	aaaaa	t tca	atctt	ttt a	atato	gtgto	t to	ggttctag	6584
act	ttcag	gctt	ttg	gaaati	g ct	aaat	agaa	a tto	caaaaa	atc 1	ctgo	catco	t ga	nggtgatat	6644
ac	ttca	tatt	tgta	aatcaa	ac to	gaaag	gagct	gto	gcatta	ata a	aaato	cagtt	a ga	atagttag	f _. 6704

6829

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185

180

- Ser Asn Lys Pro Gln Asp Phe Gln Ile Arg Val Arg Val Ile Glu Gly
  195 200 205
- Arg Gln Leu Ser Gly Asn Asn Ile Arg Pro Val Val Lys Val His Val 210 215 220
- Cys Gly Gln Thr His Arg Thr Arg Ile Lys Arg Gly Asn Asn Pro Phe 225 230 235 240
- Phe Asp Glu Leu Phe Phe Tyr Asn Val Asn Met Thr Pro Ser Glu Leu 245 250 255
- Met Asp Glu Ile Ile Ser Ile Arg Val Tyr Asn Ser His Ser Leu Arg 260 265 270
- Ala Asp Cys Leu Met Gly Glu Phe Lys Ile Asp Val Gly Phe Val Tyr 275 280 285
- Asp Glu Pro Gly His Ala Val Met Arg Lys Trp Leu Leu Leu Asn Asp 290 295 300
- Pro Glu Asp Thr Ser Ser Gly Ser Lys Gly Tyr Met Lys Val Ser Met 305 310 315 320
- Phe Val Leu Gly Thr Gly Asp Glu Pro Pro Pro Glu Arg Arg Asp Arg 325 330 335
- Asp Asn Asp Ser Asp Asp Val Glu Ser Asn Leu Leu Pro Ala Gly 340 345 350
- Ile Ala Leu Arg Trp Val Thr Phe Leu Leu Lys Ile Tyr Arg Ala Glu 355 360 365
- Asp Ile Pro Gln Met Asp Asp Ala Phe Ser Gln Thr Val Lys Glu Ile 370 375 380
- Phe Gly Gly Asn Ala Asp Lys Lys Asn Leu Val Asp Pro Phe Val Glu
- Val Ser Phe Ala Gly Lys Lys Val Cys Thr Asn Ile Ile Glu Lys Asn 405 410 415
- Ala Asn Pro Glu Trp Asn Gln Val Val Asn Leu Gln Ile Lys Phe Pro
  420 425 430

- Ser Val Cys Glu Lys Ile Lys Leu Thr Ile Tyr Asp Trp Asp Arg Leu 435 440 445
- Thr Lys Asn Asp Val Val Gly Thr Thr Tyr Leu His Leu Ser Lys Ile 450 455 460
- Ala Ala Ser Gly Glu Val Glu Asp Phe Ser Ser Ser Gly Thr Gly 465 470 475 480
- Ala Ala Ser Tyr Thr Val Asn Thr Gly Glu Thr Glu Val Gly Phe Val
  485 490 495
- Pro Thr Phe Gly Pro Cys Tyr Leu Asn Leu Tyr Gly Ser Pro Arg Glu 500 505 510
- Tyr Thr Gly Phe Pro Asp Pro Tyr Asp Glu Leu Asn Thr Gly Lys Gly 515 520 525
- Glu Gly Val Ala Tyr Arg Gly Arg Ile Leu Val Glu Leu Ala Thr Phe 530 535 540
- Leu Glu Lys Thr Pro Pro Asp Lys Lys Leu Glu Pro Ile Ser Asn Asp 545 550 555 560
- Asp Leu Leu Val Val Glu Lys Tyr Gln Arg Arg Arg Lys Tyr Ser Leu 565 570 575
- Ser Ala Val Phe His Ser Ala Thr Met Leu Gln Asp Val Gly Glu Ala 580 585 590
- Ile Gln Phe Glu Val Ser Ile Gly Asn Tyr Gly Asn Lys Phe Asp Thr 595 600 605
- Thr Cys Lys Pro Leu Ala Ser Thr Thr Gln Tyr Ser Arg Ala Val Phe 610 615 620
- Asp Gly Asn Tyr Tyr Tyr Leu Pro Trp Ala His Thr Lys Pro Val 625 630 635 640
- Val Thr Leu Thr Ser Tyr Trp Glu Asp Ile Ser His Arg Leu Asp Ala 645 650 655
- Val Asn Thr Leu Leu Ala Met Ala Glu Arg Leu Gln Thr Asn Ile Glu 660 665 670
- Ala Leu Lys Ser Gly Ile Gln Gly Lys Ile Pro Ala Asn Gln Leu Ala

Glu Leu Trp Leu Lys Leu Ile Asp Glu Val Ile Glu Asp Thr Arg Tyr Thr Leu Pro Leu Thr Glu Gly Lys Ala Asn Val Thr Val Leu Asp Thr Gln Ile Arg Lys Leu Arg Ser Arg Ser Leu Ser Gln Ile His Glu Ala Ala Val Arg Met Arg Ser Glu Ala Thr Asp Val Lys Ser Thr Leu Ala Glu Ile Glu Asp Trp Leu Asp Lys Leu Met Gln Leu Thr Glu Glu Pro Gln Asn Ser Met Pro Asp Ile Ile Ile Trp Met Ile Arg Gly Glu Lys Arg Leu Ala Tyr Ala Arg Ile Pro Ala His Gln Val Leu Tyr Ser Thr Ser Gly Glu Asn Ala Ser Gly Lys Tyr Cys Gly Lys Thr Gln Thr Ile Phe Leu Lys Tyr Pro Gln Glu Lys Asn Asn Gly Pro Lys Val Pro Val Glu Leu Arg Val Asn Ile Trp Leu Gly Leu Ser Ala Val Glu Lys Lys Phe Asn Ser Phe Ala Glu Gly Thr Phe Thr Val Phe Ala Glu Met Tyr Glu Asn Gln Ala Leu Met Phe Gly Lys Trp Gly Thr Ser Gly Leu Val Gly Arg His Lys Phe Ser Asp Val Thr Gly Lys Ile Lys Leu Lys Arg . 885

Glu Phe Phe Leu Pro Pro Lys Gly Trp Glu Trp Glu Gly Glu Trp Ile

Val Asp Pro Glu Arg Ser Leu Leu Thr Glu Ala Asp Ala Gly His Thr 

- Glu Phe Thr Asp Glu Val Tyr Gln Asn Glu Ser Arg Tyr Pro Gly Gly 930 935 940
- Asp Trp Lys Pro Ala Glu Asp Thr Tyr Thr Asp Ala Asn Gly Asp Lys 955 950 955
- Ala Ala Ser Pro Ser Glu Leu Thr Cys Pro Pro Gly Trp Glu Trp Glu 965 970 975
- Asp Asp Ala Trp Ser Tyr Asp Ile Asn Arg Ala Val Asp Glu Lys Gly 980 985 990
- Trp Glu Tyr Gly Ile Thr Ile Pro Pro Asp His Lys Pro Lys Ser Trp 995 1000 1005
- Val Ala Ala Glu Lys Met Tyr His Thr His Arg Arg Arg Arg Leu 1010 1015 1020
- Val Arg Lys Arg Lys Lys Asp Leu Thr Gln Thr Ala Ser Ser Thr 1025 1030 1035
- Ala Arg Ala Met Glu Glu Leu Gln Asp Gln Glu Gly Trp Glu Tyr 1040 1045 1050
- Ala Ser Leu Ile Gly Trp Lys Phe His Trp Lys Gln Arg Ser Ser 1055 1060 1065
- Asp Thr Phe Arg Arg Arg Arg Trp Arg Arg Lys Met Ala Pro Ser 1070 1075 1080
- Glu Thr His Gly Ala Ala Ala Ile Phe Lys Leu Glu Gly Ala Leu 1085 1090 1095
- Gly Ala Asp Thr Thr Glu Asp Gly Asp Glu Lys Ser Leu Glu Lys
  1100 1105 1110
- Gln Lys His Ser Ala Thr Thr Val Phe Gly Ala Asn Thr Pro Ile 1115 1120 1125
- Val Ser Cys Asn Phe Asp Arg Val Tyr Ile Tyr His Leu Arg Cys 1130 1135 1140
- Tyr Val Tyr Gln Ala Arg Asn Leu Leu Ala Leu Asp Lys Asp Ser 1145 1150 1155

### PCT/USOB/B711#3

- Phe Ser Asp Pro Tyr Ala His Ile Cys Phe Leu His Arg Ser Lys 1160 1165 1170
- Thr Thr Glu Ile Ile His Ser Thr Leu Asn Pro Thr Trp Asp Gln 1175
- Thr Ile Ile Phe Asp Glu Val Glu Ile Tyr Gly Glu Pro Gln Thr 1190
- Val Leu Gln Asn Pro Pro Lys Val Ile Met Glu Leu Phe Asp Asn 1205 1210 1215
- Asp Gln Val Gly Lys Asp Glu Phe Leu Gly Arg Ser Ile Phe Ser 1220 1225 1230
- Pro Val Val Lys Leu Asn Ser Glu Met Asp Ile Thr Pro Lys Leu 1235 1240 1245
- Leu Trp His Pro Val Met Asn Gly Asp Lys Ala Cys Gly Asp Val 1250 1255 1260
- Leu Val Thr Ala Glu Leu Ile Leu Arg Gly Lys Asp Gly Ser Asn 1265 1270 1275
- Leu Pro Ile Leu Pro Pro Gln Arg Ala Pro Asn Leu Tyr Met Val 1280 1280
- Pro Gln Gly Ile Arg Pro Val Val Gln Leu Thr Ala Ile Glu Ile 1295 1300 1305
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- Ile Thr Ser Pro Ser Leu Val Val Glu Cys Gly Glu Arg Val 1325 1330 1335
- Glu Ser Val Val Ile Lys Asn Leu Lys Lys Thr Pro Asn Phe Pro 1340 1345 1350
- Ser Ser Val Leu Phe Met Lys Val Phe Leu Pro Lys Glu Glu Leu 1355 . 1360 1365 .
- Tyr Met Pro Pro Leu Val Ile Lys Val Ile Asp His Arg Gln Phe 1370 1380
- Gly Arg Lys Pro Val Val Gly Gln Cys Thr Ile Glu Arg Leu Asp

1390

1395

- Arg Phe Arg Cys Asp Pro Tyr Ala Gly Lys Glu Asp Ile Val Pro 1400 1400 1405
- Gln Leu Lys Ala Ser Leu Leu Ser Ala Pro Pro Cys Arg Asp Ile 1415 1420 1425
- Val Ile Glu Met Glu Asp Thr Lys Pro Leu Leu Ala Ser Lys Leu 1430 1435 1440
- Thr Glu Lys Glu Glu Glu Ile Val Asp Trp Trp Ser Lys Phe Tyr 1445 1450 1455
- Ala Ser Ser Gly Glu His Glu Lys Cys Gly Gln Tyr Ile Gln Lys 1460 1465 1470
- Gly Tyr Ser Lys Leu Lys Ile Tyr Asn Cys Glu Leu Glu Asn Val 1475 1480 1485
- Ala Glu Phe Glu Gly Leu Thr Asp Phe Ser Asp Thr Phe Lys Leu 1490 1495 1500
- Tyr Arg Gly Lys Ser Asp Glu Asn Glu Asp Pro Ser Val Val Gly
- Glu Phe Lys Gly Ser Phe Arg Ile Tyr Pro Leu Pro Asp Asp Pro 1520 1530
- Ser Val Pro Ala Pro Pro Arg Gln Phe Arg Glu Leu Pro Asp Ser 1535 1540 1545
- Val Pro Gln Glu Cys Thr Val Arg Ile Tyr Ile Val Arg Gly Leu 1550 1560
- Glu Leu Gln Pro Gln Asp Asn Asn Gly Leu Cys Asp Pro Tyr Ile 1565 1570 1575
- Lys Ile Thr Leu Gly Lys Lys Val Ile Glu Asp Arg Asp His Tyr 1580 1585 1590
- Ile Pro Asn Thr Leu Asn Pro Val Phe Gly Arg Met Tyr Glu Leu 1595 1600 1605
- Ser Cys Tyr Leu Pro Gln Glu Lys Asp Leu Lys Ile Ser Val Tyr 1610 1620

- Asp Tyr Asp Thr Phe Thr Arg Asp Glu Lys Val Gly Glu Thr Ile 1625 1630 1635
- Ile Asp Leu Glu Asn Arg Phe Leu Ser Arg Phe Gly Ser His Cys 1640 1645 1650
- Gly Ile Pro Glu Glu Tyr Cys Val Ser Gly Val Asn Thr Trp Arg 1655 1660 1665
- Asp Gln Leu Arg Pro Thr Gln Leu Leu Gln Asn Val Ala Arg Phe 1670 1680
- Lys Gly Phe Pro Gln Pro Ile Leu Ser Glu Asp Gly Ser Arg Ile 1685 1690 1695
- Arg Tyr Gly Gly Arg Asp Tyr Ser Leu Asp Glu Phe Glu Ala Asn 1700 1705 1705
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- Leu His Ile Leu Arg Thr Gln Gly Leu Val Pro Glu His Val Glu 1730 1735 1740
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1850

1855

1860

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Ile Pro Pro Arg Leu Ile Ile Gln Ile Trp Asp Asn Asp Lys Phe 1880 1885 1890

Ser Leu Asp Asp Tyr Leu Gly Phe Leu Glu Leu Asp Leu Arg His 1895 1900 1905

Thr Ile Ile Pro Ala Lys Ser Pro Glu Lys Cys Arg Leu Asp Met 1910 1920

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Ser Leu Phe Glu Gln Lys Ser Met Lys Gly Trp Trp Pro Cys Tyr 1940 1945 1950

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